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## RAW SEQUENCE LISTING

DATE: 04/17/2001

PATENT APPLICATION: US/09/824,286

TIME: 10:47:23

Input Set : A:\A006p.txt

Output Set: N:\CRF3\04172001\I824286.raw

## SEQUENCE LISTING

ENTERED

## 4 (1) GENERAL INFORMATION:

6 (i) APPLICANT: Burkly, Linda C  
 7 Benjamin, Christopher D  
 8 Hession, Catherine A  
 9 Whitty, Adrian

11 (ii) TITLE OF INVENTION: COMMON GAMMA CHAIN BLOCKING AGENTS

13 (iii) NUMBER OF SEQUENCES: 17

15 (iv) CORRESPONDENCE ADDRESS:

16 (A) ADDRESSEE: Biogen, Inc.  
 17 (B) STREET: 14 Cambridge Center  
 18 (C) CITY: Cambridge  
 19 (D) STATE: Massachusetts  
 20 (E) COUNTRY: USA  
 21 (F) ZIP: 02142

23 (v) COMPUTER READABLE FORM:

24 (A) MEDIUM TYPE: Floppy disk  
 25 (B) COMPUTER: IBM PC compatible  
 26 (C) OPERATING SYSTEM: PC-DOS/MS-DOS  
 27 (D) SOFTWARE: PatentIn Release #1.0, Version #1.30

29 (vi) CURRENT APPLICATION DATA:

C--> 30 (A) APPLICATION NUMBER: US/09/824,286  
 C--> 31 (B) FILING DATE: 02-Apr-2001  
 37 (C) CLASSIFICATION:

34 (vii) PRIOR APPLICATION DATA:

35 (A) APPLICATION NUMBER: 60/017,466  
 36 (B) FILING DATE: 10-MAY-1996

39 (viii) ATTORNEY/AGENT INFORMATION:

40 (A) NAME: Kaplan, Warren A.  
 41 (B) REGISTRATION NUMBER: 34,199  
 42 (C) REFERENCE/DOCKET NUMBER: A006 PCT CIP

44 (ix) TELECOMMUNICATION INFORMATION:

45 (A) TELEPHONE: 617 679-2000  
 46 (B) TELEFAX: 617 679-2838

49 (2) INFORMATION FOR SEQ ID NO: 1:

51 (i) SEQUENCE CHARACTERISTICS:

52 (A) LENGTH: 1446 base pairs  
 53 (B) TYPE: nucleic acid  
 54 (C) STRANDEDNESS: single  
 55 (D) TOPOLOGY: linear

57 (ii) MOLECULE TYPE: cDNA

59 (iii) HYPOTHETICAL: NO

61 (iv) ANTI-SENSE: NO

64 (vii) IMMEDIATE SOURCE:

65 (B) CLONE: pLB001

69 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

71 ATGGTGAAGC CATCATTACC ATTCACATCC CTCTTATTCC TGCAGCTGCC CCTGCTGGGA 60

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73 GTGGGGCTGA ACACGACAAT TCTGACGCCC AATGGGAATG AAGACACCAC AGCTGATTTT 120
75 TTCCTGACCA CTATGCCCAC TGACTCCCTC AGTGTTCCTA CTCTGCCCTT CCCAGAGGTT 180
77 CAGTGTGTTG TGTTCATGT CGAGTACATG AATTGCACTT GGAACAGCAG CTCTGAGCCC 240
79 CAGCCTACCA ACCTCACTCT GCATTATTGG TACAAGAACT CGGATAATGA TAAAGTCCAG 300
81 AAGTGCAGCC ACTATCTATT CTCTGAAGAA ATCACTTCTG GCTGTCAGTT GCAAAAAAAG 360
83 GAGATCCACC TCTACCAAAC ATTTGTGTGT CAGCTCCAGG ACCCACGGGA ACCCAGGAGA 420
85 CAGGCCACAC AGATGCTAAA ACTGCAGAA CTGGTGATCC CCTGGGCTCC AGAGAACCTA 480
87 ACACTTCACA AACTGAGTGA ATCCCAGCTA GAAGTGAAGT GGAACAACAG ATTCTTGAAC 540
89 CACTGTTTGG ACACCTTGGT GCAGTACCGG ACTGACTGGG ACCACAGCTG GACTGAACAA 600
91 TCAGTGGATT ATAGACATAA GTTCTCCTTG CCTAGTGTGG ATGGGCAGAA ACGCTACATG 660
93 TTTCTGTGTC GGAGCCGCTT TAACCCACTC TGTGGAAGTG CTCAGCATTG GAGTGAATGG 720
95 AGCCACCCAA TCCACTGGGG GAGCAATACT TCAAAAGAGA ATGTCGACAA AACTCACACA 780
97 TGCCACCGT GCCCAGCACC TGAATCCTG GGGGGACCGT CAGTCTTCCT CTTCCCCCCA 840
99 AAACCCAAGG ACACCCTCAT GATCTCCCGG ACCCTGAGG TCACATGCGT GGTGGTGGAC 900
101 GTGAGCCACG AAGACCCTGA GGTCAAGTTC AACTGGTACG TGGACGGCGT GGAGGTGCAT 960
103 AATGCCAAGA CAAAGCCGCG GGAGGAGCAG TACAACAGCA CGTACCGTGT GGTGAGCGTC 1020
105 CTCACCGTCC TGCACCAGGA CTGGCTGAAT GGCAAGGAGT ACAAGTGCAA GGTCTCCAAC 1080
107 AAAGCCCTCC CAGCCCCCAT CGAGAAAACC ATCTCAAAG CCAAAGGGCA GCCCCGAGAA 1140
109 CCACAGGTGT ACACCCTGCC CCCATCCCGG GATGAGCTGA CCAAGAACCA GGTGAGCCTG 1200
111 ACCTGCCTGG TCAAAGGCTT CTATCCAGC GACATCGCCG TGGAGTGGGA GAGCAATGGG 1260
113 CAGCCGGAGA ACAACTACAA GACCACGCCT CCCGTGTTGG ACTCCGACGG CTCCTTCTTC 1320
115 CTCTACAGCA AGCTACCGT GGACAAGAGC AGGTGGCAGC AGGGGAACGT CTTCTCATGC 1380
117 TCCGTGATGC ATGAGGCTCT GCACAACCAC TACACGCAGA AGAGCCTCTC CTGTCTCCG 1440
119 GGTAAA

```

121 (2) INFORMATION FOR SEQ ID NO: 2:

123 (i) SEQUENCE CHARACTERISTICS:

124 (A) LENGTH: 482 amino acids

125 (B) TYPE: amino acid

126 (C) STRANDEDNESS: single

127 (D) TOPOLOGY: linear

129 (ii) MOLECULE TYPE: cDNA

131 (iii) HYPOTHETICAL: YES

133 (iv) ANTI-SENSE: NO

138 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

```

140 Met Val Lys Pro Ser Leu Pro Phe Thr Ser Leu Leu Phe Leu Gln Leu
141 1 5 10 15
143 Pro Leu Leu Gly Val Gly Leu Asn Thr Thr Ile Leu Thr Pro Asn Gly
144 20 25 30
146 Asn Glu Asp Thr Thr Ala Asp Phe Phe Leu Thr Thr Met Pro Thr Asp
147 35 40 45
149 Ser Leu Ser Val Ser Thr Leu Pro Leu Pro Glu Val Gln Cys Phe Val
150 50 55 60
152 Phe Asn Val Glu Tyr Met Asn Cys Thr Trp Asn Ser Ser Ser Glu Pro
153 65 70 75 80
155 Gln Pro Thr Asn Leu Thr Leu His Tyr Trp Tyr Lys Asn Ser Asp Asn
156 85 90 95
158 Asp Lys Val Gln Lys Cys Ser His Tyr Leu Phe Ser Glu Glu Ile Thr
159 100 105 110
161 Ser Gly Cys Gln Leu Gln Lys Lys Glu Ile His Leu Tyr Gln Thr Phe

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162          115          120          125
164 Val Val Gln Leu Gln Asp Pro Arg Glu Pro Arg Arg Gln Ala Thr Gln
165          130          135          140
167 Met Leu Lys Leu Gln Asn Leu Val Ile Pro Trp Ala Pro Glu Asn Leu
168          145          150          155          160
170 Thr Leu His Lys Leu Ser Glu Ser Gln Leu Glu Leu Asn Trp Asn Asn
171          165          170          175
173 Arg Phe Leu Asn His Cys Leu Glu His Leu Val Gln Tyr Arg Thr Asp
174          180          185          190
176 Trp Asp His Ser Trp Thr Glu Gln Ser Val Asp Tyr Arg His Lys Phe
177          195          200          205
179 Ser Leu Pro Ser Val Asp Gly Gln Lys Arg Tyr Met Phe Arg Val Arg
180          210          215          220
182 Ser Arg Phe Asn Pro Leu Cys Gly Ser Ala Gln His Trp Ser Glu Trp
183          225          230          235          240
185 Ser His Pro Ile His Trp Gly Ser Asn Thr Ser Lys Glu Asn Val Asp
186          245          250          255
188 Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly
189          260          265          270
191 Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile
192          275          280          285
194 Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu
195          290          295          300
197 Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His
198          305          310          315          320
200 Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg
201          325          330          335
203 Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys
204          340          345          350
206 Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu
207          355          360          365
209 Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr
210          370          375          380
212 Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu
213          385          390          395          400
215 Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp
216          405          410          415
218 Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val
219          420          425          430
221 Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp
222          435          440          445
224 Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His
225          450          455          460
227 Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro
228          465          470          475          480
230 Gly Lys

```

232 (2) INFORMATION FOR SEQ ID NO: 3:

234 (i) SEQUENCE CHARACTERISTICS:

235 (A) LENGTH: 112 amino acids

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236      (B) TYPE: amino acid
237      (C) STRANDEDNESS:
238      (D) TOPOLOGY: linear
240      (ii) MOLECULE TYPE: peptide
242      (v) FRAGMENT TYPE: internal
247      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
249      Leu Gln Glu Ser Gly Pro Gly Leu Val Ala Pro Ser Gln Ser Leu Ser
250      1          5          10          15
252      Ile Thr Cys Thr Val Ser Gly Phe Ser Leu Thr Ser Tyr Gly Val His
253      20          25          30
255      Trp Val Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Leu Gly Val Ile
256      35          40          45
258      Trp Ala Gly Gly Ser Thr Asn Tyr Asn Ser Ala Leu Met Ser Arg Leu
259      50          55          60
261      Asn Ile Asn Arg Asp Asn Ser Lys Ser Gln Ile Phe Leu Lys Met Asn
262      65          70          75          80
264      Ser Leu Gln Thr Asp Asp Thr Ala Ile Tyr Tyr Cys Ala Arg Glu Gly
265      85          90          95
267      Ser Thr Val Asp Ser Met Asp Tyr Trp Gly Gln Gly Thr Thr Val Thr
268      100         105         110
271 (2) INFORMATION FOR SEQ ID NO: 4:
273      (i) SEQUENCE CHARACTERISTICS:
274          (A) LENGTH: 106 amino acids
275          (B) TYPE: amino acid
276          (C) STRANDEDNESS: not relevant
277          (D) TOPOLOGY: linear
279      (ii) MOLECULE TYPE: peptide
281      (v) FRAGMENT TYPE: internal
286      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:
288      Asp Ile Val Met Thr Gln Ser His Lys Phe Met Ser Thr Ser Val Gly
289      1          5          10          15
291      Asp Ser Ile Thr Ile Thr Cys Lys Ala Ser Gln Asp Val Thr Thr Ala
292      20          25          30
294      Val Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile
295      35          40          45
297      Tyr Trp Ala Ser Thr Arg His Thr Gly Val Pro Asp Arg Phe Thr Gly
298      50          55          60
300      Ser Gly Ser Gly Thr Asp Tyr Thr Leu Thr Ile Ser Ser Val Gln Ala
301      65          70          75          80
303      Glu Asp Leu Ala Leu Tyr Tyr Cys Gln Gln His Tyr Ile Thr Pro Trp
304      85          90          95
306      Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile
307      100         105
309 (2) INFORMATION FOR SEQ ID NO: 5:
311      (i) SEQUENCE CHARACTERISTICS:
312          (A) LENGTH: 319 base pairs
313          (B) TYPE: nucleic acid
314          (C) STRANDEDNESS: single
315          (D) TOPOLOGY: linear

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317      (ii) MOLECULE TYPE: cDNA
322      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:
324      GATATCGTAA TGACCCAGTC TCACAAATTC ATGTCCACAT CAGTAGGAGA CAGTATCACC      60
326      ATCACCTGCA AGGCCAGTCA GGATGTGACT ACTGCTGTAG CCTGGTATCA ACAAAAACCA      120
328      GGGCAATCTC CTAAACTTCT GATTTACTGG GCATCCACCC GGCACACTGG AGTCCCTGAT      180
330      CGCTTCACAG GCAGTGGATC TGGGACAGAT TATACTCTCA CCATCAGCAG TGTGCAGGCT      240
332      GAAGACCTGG CACTTTATTA CTGTCAGCAA CATTATATCA CTCCGTGGAC GTTCGGTGGA      300
334      GGGACCAAGC TGGAGATCT      319
336 (2) INFORMATION FOR SEQ ID NO: 6:
338      (i) SEQUENCE CHARACTERISTICS:
339          (A) LENGTH: 336 base pairs
340          (B) TYPE: nucleic acid
341          (C) STRANDEDNESS: single
342          (D) TOPOLOGY: linear
344      (ii) MOLECULE TYPE: cDNA
349      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:
351      CTGCAGGAGT CAGGACCTGG CCTGGTGGCG CCCTCACAGA GCCTGTCCAT CACTTGCACT      60
353      GTCTCTGGGT TTTTATTAAC CAGCTATGGT GTACACTGGG TTCGCCAGCC TCCAGGAAAG      120
355      GGTCTGGAGT GGCTGGGAGT CATTGTTGGCT GGTGGAAGCA CAAATTATAA TTCGGCTCTC      180
357      ATGTCCAGAC TGAACATCAA CAGAGACAAT TCCAAGAGCC AAATTTTCTT AAAAATGAAC      240
359      AGTCTGCAAA CTGATGACAC AGCCATCTAC TACTGTGCCA GAGAGGGTTC TACGGTAGAT      300
361      TCTATGGACT ACTGGGGCCA AGGGACCACG GTCACC      336
363 (2) INFORMATION FOR SEQ ID NO: 7:
365      (i) SEQUENCE CHARACTERISTICS:
366          (A) LENGTH: 36 base pairs
367          (B) TYPE: nucleic acid
368          (C) STRANDEDNESS: single
369          (D) TOPOLOGY: linear
371      (ii) MOLECULE TYPE: cDNA
376      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:
378      AACTGCAGCG GCCGCCATGG TGAAGCCATC ATTACC      36
380 (2) INFORMATION FOR SEQ ID NO: 8:
382      (i) SEQUENCE CHARACTERISTICS:
383          (A) LENGTH: 32 base pairs
384          (B) TYPE: nucleic acid
385          (C) STRANDEDNESS: single
386          (D) TOPOLOGY: linear
388      (ii) MOLECULE TYPE: cDNA
393      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:
395      GACTTTGTCG ACATTCTCTT TTGAAGTATT GC      32
397 (2) INFORMATION FOR SEQ ID NO: 9:
399      (i) SEQUENCE CHARACTERISTICS:
400          (A) LENGTH: 27 base pairs
401          (B) TYPE: nucleic acid
402          (C) STRANDEDNESS: single
403          (D) TOPOLOGY: linear
405      (ii) MOLECULE TYPE: cDNA
410      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:
412      CTGGATATCG TAATGACCCA GTCTCCA      27

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VERIFICATION SUMMARY

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L:30 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]

L:31 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]